

**Table S1.** Dimerization capabilities of mutagenized STS1, J-PI, and ZMM18

<b>Backbone</b>	<b>63<sup>1</sup></b>	<b>65</b>	<b>73</b>	<b>81</b>	<b>82</b>	<b>Dimerization<sup>2</sup></b>
STS1	Ser	Ser	Thr	Gly	Glu	Ob. Het. <sup>3</sup>
STS1	<b>Thr</b>	Ser	Thr	Gly	Glu	Ob. Het.
STS1	Ser	<b>Pro</b>	Thr	Gly	Glu	Ob. Het.
STS1	Ser	Ser	<b>Ile</b>	Gly	Glu	Ob. Het.
STS1	Ser	Ser	Thr	<b>Asp</b>	Glu	<b>Ho.</b>
STS1	Ser	Ser	Thr	Gly	<b>Asp</b>	Ob. Het.
STS1	<b>Thr</b>	<b>Pro</b>	Thr	<b>Asp</b>	<b>Asp</b>	<b>Ho.</b>
STS1	<b>Thr</b>	<b>Pro</b>	Thr	<b>Asp</b>	Glu	<b>Ho.</b>
STS1	Ser	<b>Pro</b>	Thr	<b>Asp</b>	<b>Asp</b>	<b>Ho.</b>
STS1	<b>Thr</b>	Ser	Thr	<b>Asp</b>	<b>Asp</b>	<b>Ho.</b>
STS1	<b>Thr</b>	<b>Pro</b>	Thr	Gly	<b>Asp</b>	Ob. Het.
STS1	<b>Thr</b>	<b>Pro</b>	Thr	Gly	Glu	Ob. Het.
STS1	Ser	<b>Pro</b>	Thr	<b>Asp</b>	Glu	<b>Ho.</b>
STS1	Ser	Ser	<b>Ile</b>	<b>Asp</b>	Glu	Ob. Het.
STS1	Ser	Ser	Thr	<b>Asp</b>	<b>Asp</b>	Ob. Het.
STS1	<b>Thr</b>	Ser	Thr	<b>Asp</b>	Glu	<b>Ho.</b>
STS1	<b>Thr</b>	Ser	Thr	Gly	<b>Asp</b>	Ob. Het.
STS1	Ser	<b>Pro</b>	Thr	Gly	<b>Asp</b>	Ob. Het.
J-PI	Thr	Pro	Asp	Asp	Asp	Ho. <sup>3</sup>
J-PI	Thr	Pro	<b>Gly</b>	<b>Gly</b>	Asp	<b>Ob. Het.</b>
ZMM18	Ser	Ser	Gly	Gly	Glu	Ob. Het. <sup>3</sup>
ZMM18	Ser	Ser	<b>Asp</b>	<b>Asp</b>	Glu	Ob. Het.

<sup>1</sup> Amino acid residue position in STS1. Wild-type identities are shown in regular print, residue identities in **bold** indicate mutagenesis. <sup>2</sup> Ob. Het. = Bound DNA probe as obligate heterodimers with AP3<sup>L</sup> proteins in gel shift assays. Ho. = capable of binding DNA probe as a homodimer in gel shift assays. Results in **bold** indicate transitions between obligate heterodimerization and homodimerization and vice versa.

<sup>3</sup> Results reported in (Bartlett, et al. 2015; Whipple, et al. 2004; Whipple and Schmidt 2006)